

Docket No.: PC-0034 US

CERTIFICATE OF FACSIMILE TRANSMISSION

I hereby certify that this paper is being facsimile transmitted to the attention of Examiner O. Chernyshev, Group Art Unit 1646, Box Non-Fee Amendment, U.S. Patent and Trademark Office to Facsimile No. 703-782-9306 on October 10, 2002.

By:

Printed: Margaret M. Hasson

703-782-9303

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Jennifer L. Hillman

FAX RECEIVED

OCT 11 2002

Title: TIMM8b-RELATED PROTEIN

GROUP 1600

Serial No.: 09/781,117

Filing Date: February 08, 2001

Examiner: Chernyshev, O.

Group Art Unit: 1646

Box Non-Fee Amendment
 Commissioner for Patents
 Washington, D.C. 20231
 Attn: Examiner Olga N. Chernyshev

TRANSMITTAL FEE SHEET

Sir:

Transmitted herewith are the following for the above-identified application:

1. Return Receipt Postcard;
2. Response to Office Action (10 pp.);
3. Copy of Return Receipt Postcard dated 02/01/01);
4. Copy of Tables 1 and 2 (2 pp.);
5. Breener et al. reference (pp. 6073-6078); and
6. Exhibit A (1 pg.).

The fee has been calculated as follows:

Claims	Claims After Amendment	Other Previously Paid For	Pending Claims	Other Than Small Entity Rate	Additional Fee(s)
Total	20	.	20	= \$18.00	\$ 0
Indep't	2	.	3	= \$584.00	\$ 0
				Total Fee: \$ 0	

 No additional Fee is required.

The Commissioner is hereby authorized to charge any additional fees required under 37 CFR 1.16 and 1.17, or credit overpayment to Deposit Account No. 09-0108. A duplicate copy of this sheet is enclosed.

Respectfully submitted,

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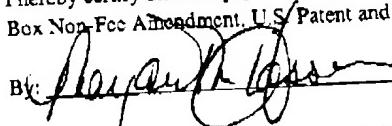
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By:  Printed: Margaret M. Hasson
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RESPONSE TO OFFICE ACTION

Sir:

This paper is responsive to the Office Action dated July 11, 2002, Applicant(s) request reconsideration of the above-referenced patent application in view of the following amendments and remarks.

IN THE SPECIFICATION

Please replace the paragraph beginning at p. 28, line 10 with the following rewritten paragraph:
The BLAST software suite (NCBI, Bethesda MD), includes various sequence analysis programs including "blastn" that is used to align nucleotide sequences and BLAST2 that is used for direct pairwise comparison of either nucleotide or amino acid sequences. BLAST programs are commonly used with gap and other parameters set to default settings, e.g.: Matrix: BLOSUM62;

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